

```

humPMS2 (2574) 2661 CATTCTCAGAAC-----2730
AtPMS2 (2267) CTTTACTCACTTACCTGATGACGACAATGTCAATGATGATGATGATGATGATGCAACCATCTCATTGGC
Consensus (2661) C TT CTCA A
humPMS2 (2587) ----
AtPMS2 (2337) ATGA
Consensus (2731)

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Figure 1. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) DNA sequences. Similarity is 48.1%; identity is 48.1%. Black boxes show identical nucleotides.

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1                                     70
humPMS2 (1) --MERAEESSTEPAKAIKEFDKSVHQICSGOVVLSSTAVKELVENS LDAGATNIDLKIKOYGVLLIEV
AtPMS2 (1) MQGDSSPPTITSSPLIRPINNVIRICSGQVILDLSSAVKELVENS LDAGATSTEINLRDYGEYFQV
Consensus (1) D A S S T A IKPI R IH ICSGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V
71                                     140
humPMS2 (69) SDNGCGVEEENF-----EGTILFHTSKIQEFADLTQVETFGFRGEALSSLCALSDVTISCHA
AtPMS2 (71) IDNGCGISPTNFKVCVQILRRTFDVLALFHTSKLEDFIDILNLTTFGFRGEALSSLCALGNLTVEIRTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSLCAL LTI T
141                                     210
humPMS2 (128) SAKVGTREMFDFHNSKIIQKTPYPRPGTTVSQQQLFSTLPVRHKEFORNIKEYAKMVOVLHAYCISAG
AtPMS2 (141) NEPVATLTFDHSGLLTABKKTARQIGTTTTRKLFSLNLPVRSKEFKENIRKEYCKLVSLLNAYALAKG
Consensus (141) VAT L FDH G I R GTTVSV LFS LPVR KEF RNIKEYAKLV LL AY IIA G
211                                     280
humPMS2 (198) IRVSGTNOLCGQKRQPVVCTGSPSIRKEGGSVFGQKQLQSLIFVQLPPSDSVCEEYGLSCSDALHNL
AtPMS2 (211) VRFVCSNITCKNPKSVVLNTQGRGSLKDIITVFGISTFTSQQ-----
Consensus (211) IR CSN G K VL T G STKDNISVFG SL P
281                                     350
humPMS2 (268) YISGFISQCTHGVGRSSTDRQFFFINRRCDPAKVCRLVNEVHEMYNRHOYFVVNLNISVDSECVINVT
AtPMS2 (255) ---G-----TGNLADRCVFFINGREVDMKVKSLVNELKDTSSRKVFVTILDFIVPGGACILNVT
Consensus (281) G GR DRQFFFIN RP D KV KLVNELY YP IL V DINVT
351                                     420
humPMS2 (338) PDKRQIILQEEKLLLAVALKTSLIGMFDSDVNKLNVSQQLLDVEGNLIKMHAAADLEKPMVEKQDQSPSLR
AtPMS2 (314) PDKRKVFFSDET-----SV-----
Consensus (351) PDKR I DE
421                                     490
humPMS2 (408) TGEKKDVSISRLREAFSLRHTTENKPHSPKTFEPRRSPIGQKRGMLSSSTSGAISDKGVLRPQKEAVSS
AtPMS2 (328) -----IGSLREGLNEIYSSSNASYIVNRFENSEQPDKAGVSSFQKKSNNLLSEGIVLDVSSKTRLG
Consensus (421) I LREA HSS N H E S ISD VL
491                                     560
humPMS2 (478) SHGPSDPDTRAEEVKLSGHGSTSVDSSEGFSPIDTGSCHCSSEYAASSPCDRGSQEHVDSQEKAPETDCSFS
AtPMS2 (389) EAIEKENPSLREVEIDNSSPMEKFKFEIKACGTKKGEGLSVHDVTHLDKTPSKGLPQLNVTEKVIDASK
Consensus (491) D EVE D E A S S DK L DA
561                                     630
humPMS2 (548) DVDCHSNQEDTGCKRVLVLPQPINLATPNTYRFKKEBELSSSDICQKLVNTQDMSASQVDVAVKINKKVP
AtPMS2 (459) DLSSRSS-----EAQSTLNFVTMTGKRSHENISTILSETPVLNRQTSSYRVEKSKFVRALASRCLVE
Consensus (561) DL S F T L K ILS S I S M S DV K LV
631                                     700
humPMS2 (618) LDFSMSSSLAKRIKQLHHEAQOSECEQNYRKFRAKICPGENQAEDLRKEISKTMFAEMEIIIGQFNLGFI
AtPMS2 (522) GEQLDDMVISKEDMTPSERDSELGNRISPTQA-----D-----NVERHERVILGQFNLGFI
Consensus (631) D L K E G A M IIGQFNLGFI
701                                     770
humPMS2 (688) ITKLNEDIFIVDQHAIDERYNFEMIQHVLQGRRIAPQTLNITAVNEAVLIENLEIRKNGFDVVIDE
AtPMS2 (573) IAKIERDIFIVDQHAADKFNFEHLARSVLNQCPQLQPLNLEISPEBEVTVLMHMDITENGFLLEENP
Consensus (701) I KL DIFIVDQHA DEKFNFE L TVLN Q LI P L LS E LI LDI R NGF
771                                     840
humPMS2 (758) NAEVTERAKIISLETSKNWTFGQDVDELTFMSDSPGVMC-----PSRVKQMEASRACK
AtPMS2 (643) SAPPGKHFRRAIPYSKNITFGVECLKDLSLTCGNHGECSVASSYKTSKTDSIQPSRVKRAMLASRACS
Consensus (771) AP KL AIP SKN TFG DL DLI L D G PSRVK M ASRACR
841                                     907
humPMS2 (815) SVMIGTALNTSEMKKLITFMGEMDHPWNCPHGRPTMRHIANGVISQN-----
AtPMS2 (713) SVMIGDPARKNEMQKIVEHLADLES PWNCPHGRPTMRHLVDLTLLTLPPDDDNVND DDDDDATISLA
Consensus (841) SVMIG L EM KII HLADLD PWNCPHGRPTMRHI L I

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Figure 2. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) amino acid sequences. Similarity is 41.5%; identity is 31.1%. Black boxes show identical residues.

1 70

humPMS2 (1) -----MERAESSS-----EPAKAIKPIDRKSWHOICSECVLSLSTAVKELVENSLEAGATNIDL

AtMLH1 (1) MIDSSSLTABMEEBESPARTIVPREPPKIQRLSESVNRIAAEETIQRPVSAVKELVENSLEADSSISV

Consensus (1) ME ES AT I ID V I AG VI SAVKELVENSLEA AS I L

71 140

humPMS2 (57) KLKHYGVDLIEVSLNGCCVEEENFEGLTLKHTTSKIQEFADLTQVETFGFRGEALSSLCALSDVISTICH

AtMLH1 (71) VVKDGGLKLIQVSDDGHSIRREDLPILCERHTTSKLTKEFDLFSLSMGERGEALASMTYVAHVVTITIT

Consensus (71) LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST

141 210

humPMS2 (127) ASAKVETLMFDHNGKIIQKTPYPRPGCTVSVQQLFSTLPVHEEFGRNIKKENAKMNOVLHAYCHISA

AtMLH1 (141) KGQIHGYVSYRDGVMEHEPKACAIVKGTQIMVENLEYNMIARRETLGNSADDYGRINDLSRMATHYN

Consensus (141) G RL F KGT I V NLF L R K Q N DYAKIV LL I

211 280

humPMS2 (197) GIRVSCINQLGQKRPVICTGGSPSIKENIGSVFGQKQLQSIPFVQLPPSDSVCEEYGLSCSDALHNL

AtMLH1 (210) NVSHSCRKH---CAVKADVHSVSPSRLDSIRSVYGVSVAKNIM---KV---E-----VSSCSGGCT

Consensus (211) I SC G V S SPS D I SVFG LI L LS DA

281 350

humPMS2 (267) FYISGFISQCTHGVGRSSTDQRQFFFINRPPCDPAKVCRLVNEVSHM-YNRHQYPFVVLNHSVDSGCVDIN

AtMLH1 (264) EDMEGFISNSNYVAKKTIL---VLFINDRLVECSALKKAIEIVAAATLPKASKPFVYMSINLPREHVDIN

Consensus (281) F I GFISN H KS FIN R D A L R I VY K PFV L I L E VDIN

351 420

humPMS2 (336) VTFQRQILLQEEKLLAVLKTSLIGMFDSVKNLNVSQPLLDVEGNLIIMHADLEKPMVEKQDQSPS

AtMLH1 (331) IHFTKKEVSLNQEIIEIMIQ-----SEVE-----VILRNENDTRTFQKQVEYIQ

Consensus (351) I P KK I L III MI S IKL A K E

421 490

humPMS2 (406) LRTGEEKQVSIIRLREAFSLRHTTENKPHSPKTPPEPRRSILQKRGMLSSSTSGAISDKGVLRPQKEAV

AtMLH1 (377) STLTSGSDSPVSKPSG---QKQKQVNVNKMVRTDSSDAARLHAFLQPKPQSLPDKVSSLSVVRSSV

Consensus (421) K D IS A T P P G A L L K AV

491 560

humPMS2 (476) SSSHGSDPTIRAEVEKDSGHGSTSVDSSEGSIPDTGSHCSSEYAASSPGDRGSCHEHVDSEKAPETDS

AtMLH1 (443) RQRNPKETALSSVQE-----LIA--G-----V-DSCHPCMLETVRNCTYVGMADDV

Consensus (491) P D D A V I S G E V DD

561 630

humPMS2 (546) FSDVDCHSNQEDTGCKFRVLPOPTNLATPNTKRFKKEEILSSSDICQKLVNTQDMSASQVDVAVKINKKV

AtMLH1 (489) FALVQYN---THLYLAN-----VVNLSEKLMYQOTLRRFAHFNAIQLSDPAPLSELILLALKEEDL

Consensus (561) FA V T SK L N I S S L L L

631 700

humPMS2 (616) VFLDFSMSSIAKRIKQLHHEAQOSEGEQNYRKRAKICPGENQAAEDELKKEISKTFPAEMIIIGQFNLG

AtMLH1 (547) DEGNDTKDDLKERIAEMNTELLKEKAEMLEBYSVHVDSSANLSRLPVILDQYTPMDRVVPFL--LCLG

Consensus (631) P S L RI L E AE F I NA I S M E I LG

701 770

humPMS2 (686) FIITKLNEIDIFVDQHAATDEKYNFEMLQOHTVLQQRLLIAPOTLNLTAVNEAVLLENLEIFRKNGFVFI

AtMLH1 (615) NDVEWEDKSCFQGVSAIAGNFYAMHPPLLPNPSGDGIQFYSKRGESSQEKSDIEGNVDMEDNLDQILLS

Consensus (701) I E A F G I SA A L NLDI D L

771 840

humPMS2 (756) ENAPVTERAKLISLPTSKNVTFGPDVDDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMIGTALNTS

AtMLH1 (685) EAENAWAQR-----EWSIQHVLFPMSRLFLKPPFASMASNGTFVKVASLEKLYKIFERC-----

Consensus (771) D R WS L L M S VK K K

841 877

humPMS2 (826) EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN

AtMLH1 (738) -----

Consensus (841) -----

Figure 3. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue MLH1 (AtMLH1) amino acid sequences. Similarity is 30%; identity is 18.4%. Black boxes show identical residues.

09749601-133800

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humPMS2 (1) MERAESSSTEPAKAIKIDRKSVMQICSGQVVLSTLSTAKELVENSIDAGATNIDLKLKDYGVDLIEVSD 70
AtPMS1 (1) -----MKTIKALPEGVRISMRSQIIMFDMARVVELVFNSLDAGATKVSIFVGVVSCS-VKIVD
Consensus (1) K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D

humPMS2 (71) NGCGVEENFEGTLTKHHTSKIQEADL-QQVETFGFRGEALSSLCALSDVTIS-CHASAKVGTILMFDH 140
AtPMS1 (59) DSCGVSRDDLVLGERYATSKFHD-TNVE-ASETFGFRGEALASISDISLLEVR-KAIGRPNCY-KVMKG
Consensus (71) G GV D L KH TSK DF L T ETTFGFRGEALASI IS L I T G R M

humPMS2 (140) NGKIIQKTPYFRP-RGTTVSVQQLFSTLFPVRHKEFORNIKKKEYAKMVQVLHAYCIIISAGI----- 210
AtPMS1 (129) SKCLHLGIDDDRKDSGTTVTVRDLHYSGFVRVRKYMSSPKVLESIKKCVFRIALVHSNVFSVLDIESD
Consensus (141) I R GTTVSV LF S PVR K Q KK I L II A I

humPMS2 (199) -----RVSCTNQLGQGRQPVVCTGGSPSIKENISV 280
AtPMS1 (199) EELFQTNPSSSAFSLMRDAGTEAVNSLCKVNVTDGMLNVSGFECADDWPTDQQTGRNRRLQSNPSYI
Consensus (211) VS K TG I N G I

humPMS2 (231) -----FGQKQLQSLIFVQLP-SDSVCEBYGLSCSDALHNFYISCFISQCTHGVGRSSTDRQF 350
AtPMS1 (269) LCIACPRLRYE-SFEPKTHVEFKWGVLAFTIRITLANWKKDRI-ELPDCGADILAKDRQDLIEDKI
Consensus (281) F S I F P A E LA L G G D

humPMS2 (290) FFIIR-----RPCDPAKVCLRVNEVYHMYNRHQYEFVVLNISVSECVDINVTDPKRQILL 420
AtPMS1 (339) RLQNGSLFSILHFLDADWPEAMEPAKKLKRSDHAPCSSLFP-SADFKQDGYFSPRKDWSPCEVEV
Consensus (351) N DPAK H FP D V I L

humPMS2 (346) QEEKLLLAVALKTSLIGMDSOVNKLNVSCPLLEVEGNLIKMHADLEKPMVEK-DQSPSLRTGEEKKDV 490
AtPMS1 (409) KIQNPKEQGTVAGFESRTDSLQSRDIEMTINEDFPQVTDLLLETSLVADSKCR-FLTRCQITTPVNIH
Consensus (421) DS LN I Q D L A L KQ S T

humPMS2 (416) SISRLREAFS-----LRHTTENKPHSEKTPEPRRSLPLGQ 560
AtPMS1 (479) DFMKDSVLFNFQFQGLKDELVDVSNICGKHLRGCSRVSLTFHEBPKSEVEGYESVVMIMENKQSSPRV
Consensus (491) K D L H P P K S

humPMS2 (450) KRGMLSSTSGAISDKGVLRPQKEAVSSSHG--SDPTDRAEVEKDSGHGSTSVSEGESIPTGSHCSS 630
AtPMS1 (549) LETREGCSYCDVYSRPTDCSLGSSWQDWDWFTQCSSDRGCGVIGEDFNIPISTABEDSYDEKVGSKK
Consensus (561) S SDK A S P SDRA V T IDS F D

humPMS2 (518) EYAASSPDRGSQEHVDSCF-----KAPETDSSFSQVDCHSNQEDTGCKFRVLEOPTNLATPNTKRFKKE 700
AtPMS1 (619) YLSSVNVGSSVTGSFCLSEWSPMYSTGATKWESEYQKGRILEQSLRLGRMEDPEFCFSAANNIKFDH
Consensus (631) AA G S S E P SD D K LP P S

humPMS2 (583) EILSSSDLCQKLVNTQDMSASQVDVVKANKK---VVPLDFSMSSLAIRIKQLHHEAQSECEENYRK 770
AtPMS1 (689) EVIPEMDCCETGTDSTAIQNTCLADKCKSSWGHADDVRIDQYSIRKEKFSYMDGTNNASKRKRK
Consensus (701) EII D C S LA KI K L SI K QN G Q KK

humPMS2 (649) RAKICPGENQ----- 840
AtPMS1 (759) RSAPFFYREKKRIFSLCKSDTKPKNSDPSEPDLECLTQPCNASQMHLCISILDVSYDHIQETEKRLS
Consensus (771) RA

humPMS2 (659) ----- 910
AtPMS1 (829) SASDLKASAGCRTVHSETQDEDVHEDFSSEEFDPKSTTKWRHNCAVSQVPKESHELHGQDGVFDISSG
Consensus (841)

humPMS2 (659) -----AADELKREISKTMFAEMEIIIGFNLGFIITKLNEIFLVDQHADEKYNFEMIQOHTVLQGGRL 980
AtPMS1 (899) LLHLRSDSLVPESINRHSLEDAKVLCQVDKKYPIVACGTVALVDQHAADERIRLEERTKFINDAALI
Consensus (911) A E L I K D II Q FI I IVDQHA DEK E L I A I

humPMS2 (724) IAPQTLNTAVNEAVLIENLEIFRKNFDFVIDENAPVTERAK-----LISLETSKNWTFGPQ 1050
AtPMS1 (969) FVLTLKVLPEMGYQLQSYSEQIRDWGICNIIVEGSTSPFKKNMSIIQRKPTPITNAVECILGVNLSDV
Consensus (981) L M LL E R GF I A S K L ALP

humPMS2 (782) DVDLIFMLSDSPGVMCRPSRVKQMFASRACRKSVMICITANTSEMKKLITHMGEMDHPWNCPHGRPTMR 1120
AtPMS1 (1039) DLLFLQQLATDGSSTIIPSVLRVLNSKACGAIMFGDSLPSLCSLIIDGLKQTSLSLCAHGRPTTV
Consensus (1051) DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT

humPMS2 (852) HIANGVISON----- 1164
AtPMS1 (1109) PLVDLAKLHKQIAKLSGRQVWHGLQRREITLDRAKSRLDNAKS-
Consensus (1121) I L I N

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Figure 4. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue PMS1 (AtPMS1) amino acid sequences. Similarity is 24.4%; identity is 15%. Black boxes show identical residues.

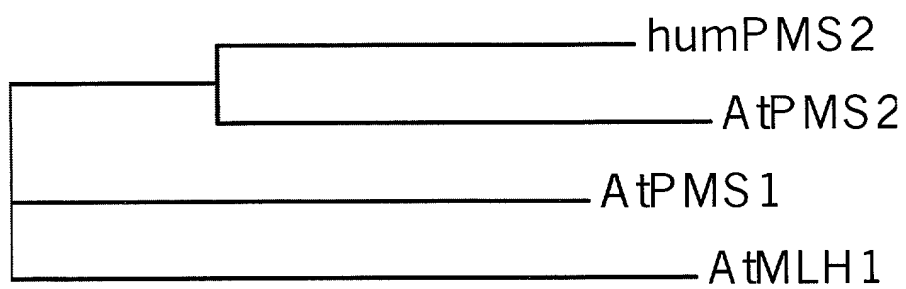


Figure 5. Phylogenetic tree of the *Arabidopsis thaliana* *PMS2* gene homologues.

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humPMS134      1
AtPMS134      1
Consensus      1
(1) ATGGGCGAGCTGAGAGCTCGAGTACAGAACCTGCTAAGGCG-----ATCAAACCTATTGTCGGAAGT
(1) ATGCGAGGAGATTCTTCTCCGCTCTCCGAGCACTACTAGCTCTCCTTTGATAAGACCTATAAACAGAAACG
(1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
71
humPMS134      71
AtPMS134      71
Consensus      71
(65) CAGTCCATCAGATTGCTCTGCGCAGGTGGTACTGAGTCTAAGCACTGCGGTAAAGGAGTTAGTAGAAAA
(71) TAATTACAGAAATCTGTTGCGCTCAAGTCACTAGACCTCTCTTCCGCCCTCAAGGAGCTTCTCAGAA
(71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA
141
humPMS134      141
AtPMS134      141
Consensus      141
(135) CAGTCCATCAGATTGCTCTGCGCAGGTGGTACTGAGTCTAAGCACTGCGGTAAAGGAGTTAGTAGAAAA
(141) TAGTCTCGACGCCCGCGCCAGCAGTATAGAGATTAACTCCGAGACTACGCCCAAGACTATTCTCAGCTC
(141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT
211
humPMS134      211
AtPMS134      211
Consensus      211
(205) TCAGACAATGGAATGTTGGGT-----AGAAGAAG-----AAAACTTCCAAGG-CTTAA-
(211) ATTGACAATGCTTGTGGCAATTTCCCAACCAATTTCAAGGTTTGTGTCCAATTTCTCGAAGAACTTTTG
(211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT
281
humPMS134      281
AtPMS134      281
Consensus      281
(251) -----CTCTGAAACATCAACATCTPAAGATTCAAGACTTGCCGACCTAACCTAGGTTGAA-ACCT
(281) ATGTTCTTGCACCTTACCATCATCTCTCTAAATAGAGGATTCACAGATCTTT-CAATTTGACTACTT
(281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT
351
humPMS134      351
AtPMS134      351
Consensus      351
(311) TTCGCTTTTCGGGCGGAAGCTCTGAGCTCACTTTGTGCACTGACCGATGTCACCACTTCTACCTG--CCAC
(350) ATGCTTTTACAGGAGGAAGGCTTGAGCTCTCTCTGTGCACTTGGGAAATCTCACTGCGGAAACAAAGACAA
(351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A
421
humPMS134      421
AtPMS134      421
Consensus      421
(379) CCATCGCGCAAGGTTTGAAGT---
(420) CAATGAGCA--GTGCTACGCTC
(421) G AT GC A GTTG AC

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Figure 6. Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) DNA sequences. Similarity is 53.2%; identity is 53.2%. Black boxes show identical nucleotides.

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1                                     70
humPMS134 (1) --MERARSSSEPAKAKKPIIDKSVHICSGQVLSLSTAVKELVENS LDAGATNIDLKLDYGVLLIEV
AtPMS134 (1) MQGDSSPSPTTSSPLIRPNNVNIHICSGQVILDLSSAVKELVENS LDAGATSI EINI RDYGEYFQV
Consensus (1) D A S ST A IKPI R IH ICSGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V

71                                     140
humPMS134 (69) SDNGCGVEEENF-----ECITLKHHTSKIQEFADLTQVEFGFRGEALSSLCALSDVTISTCHA
AtPMS134 (71) IDNGCGISPTNFKVCVQILRRTFDVIALKHHTSKLEDFTDLLNLTFGFRGEALSSLCAIGNLVETRTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSLCAL LTI T

141
humPMS134 (128) SAKVGT
AtPMS134 (141) NEPVAT
Consensus (141) VAT

```

Figure 7. Alignment between human PMS134 (humPMS134) and *Arabidopsis thaliana* homologue of PMS134 (AtPMS134) amino acid sequences. Similarity is 65.1%; identity is 50.7%. Black boxes show identical residues.

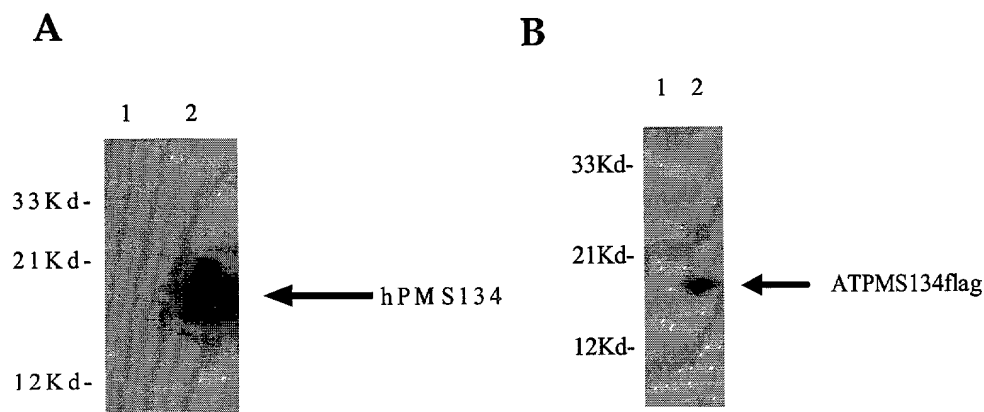


Figure 8: Western blot analysis of bacteria expressing the human PMS134 dominant negative gene (Panel A, lane 2) or the *Arabidopsis thaliana* dominant negative gene (Panel B, lane 2). Panel A, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the human PMS2 N-terminus. Panel B, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the flag epitope placed on the C-terminus of the *Arabidopsis* PMS134 gene. Lane 1 is bacteria containing empty vector as negative control

Dominant Negative Effects of *Arabidopsis thaliana* PMS2 homolog

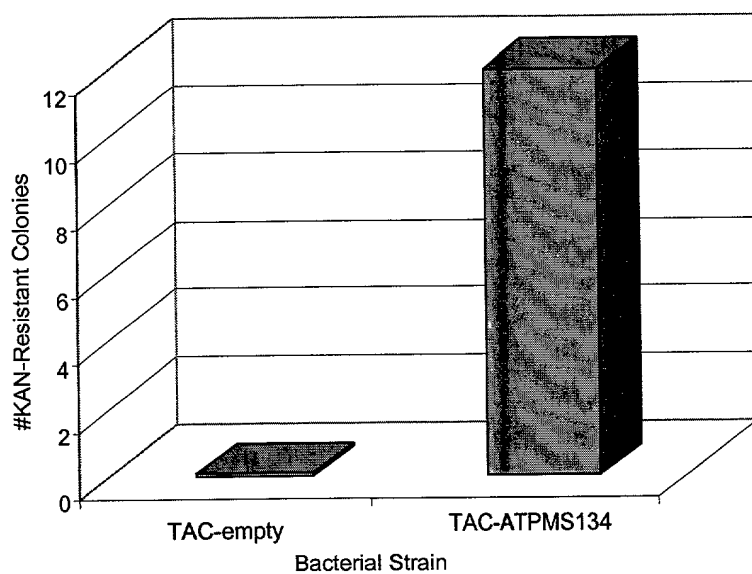


Figure 9. Expression of the *Arabidopsis thaliana* PMS134 gene produces hypermutability in bacteria leading to the generation of new phenotypes. Briefly, bacteria containing the empty vector or the TAC ATPMS134 expression vector were grown and plated on kanamycin containing Lbagar plates. The host bacteria are susceptible to KAN bactericidal activity. Bacterial cultures expressing the hPMS134 gene resulted in genetic alteration of the bacterial host and the generation of clones that are KAN resistant.

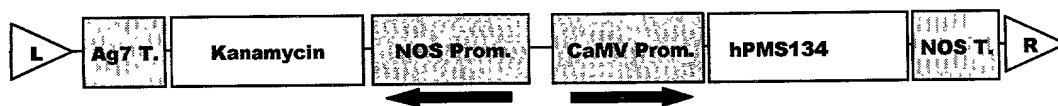


Figure 10. Schematic map of the pCMV-hPMS134-Kan binary plant expression vector. Ag7 T. and NOS T. = gene 7 and Nopaline Synthase poly(A) signals, respectively. NOS Prom and CaMV Prom = Nopaline Synthase and Cauliflower Mosaic Virus promoters, respectively. L and R = left and right T-DNA border repeats, respectively. Arrows indicate direction of transcription.

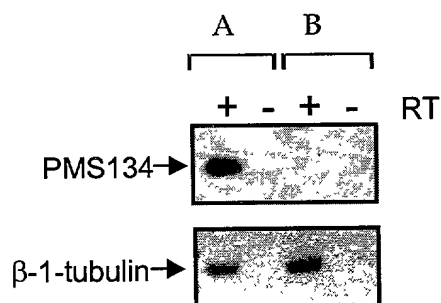


Figure 11. Expression of hPMS134 in Arabidopsis Thailana. Message analysis for T1 plants shows steady state expression of dominant negative MMR genes in PMS134-Kan plants (A) while none is observed in control plants (B). Tubulin was used as an internal control to monitor sample loading and integrity.

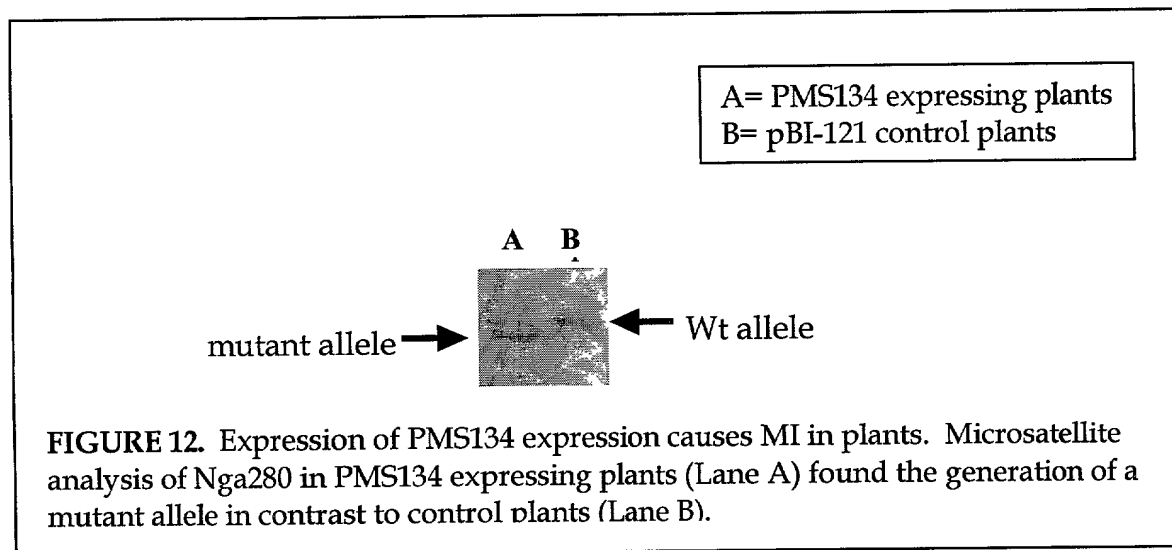


Figure 13. The plant on the left is a wild type *A. thaliana* and the one on the right is MMR defective. Seeds from the MMR defective plant have been obtained and offspring have the same “double-meristem” trait.

